CLAIMS

What is claimed is:

1. A universal integration and expression vector competent for stably transforming the chloroplast genome of different plant species which comprises an expression cassette which comprises, operably joined, a heterologous DNA sequence coding for a molecule of interest and control sequences positioned upstream from the 5' and downstream from the 3' ends of the coding sequence to provide expression of the coding sequence in the chloroplast genome of a target plant, and flanking each side of the expression cassette, flanking DNA sequences which are homologous to a spacer sequence of the target chloroplast genome, which sequence is conserved in the chloroplast genome of different plant species, whereby stable integration of the heterologous coding sequence into the chloroplast genome of the target plant is facilitated through homologous recombination of the flanking sequences with the homologous sequences in the target chloroplast genome.

2. A universal integration and expression vector competent for stably transforming the chloroplast genome of different plant species which comprises an expression cassette which comprises, operably joined, a heterologous DNA sequence coding for a peptide of interest and control sequences positioned upstream from the 5' and downstream from the 3' ends of the coding sequence to provide expression of the coding sequence in the chloroplast genome of a target plant, and flanking each side of the expression cassette, flanking DNA sequences which are homologous to a spacer sequence of the target chloroplast genome, which sequence is conserved in the chloroplast genome of different plant species, whereby stable integration of the heterologous coding sequence into the chloroplast genome of the target plant is facilitated through homologous recombination of the flanking sequences with the homologous sequences in the target chloroplast genome.

3. The vector of claim 2 which comprises a heterologous nucleotide sequence coding for a selectable phenotype.

4. The vector of claim 3 wherein the flanking sequences comprise, each one a portion of the intergenic spacer 2 region between the $tRNA^{Ile}$ and the $tRNA^{Ala}$ genes of the chloroplast genome, whereby double homologous recombination with the conserved spacer 2 region in the target chloroplast genome is facilitated.

5. The vector of claim 4 wherein the flanking sequences comprise each one in addition to the portion of the spacer region, part or all of the $tRNA^{Ile}$ and the $tRNA^{Ala}$ genes, respectively.

6. The vector of claim 5 wherein the flanking sequences comprise each one in addition to the portion of the spacer region, part or all of the 16S and/or 23S rRNA gene sequences.

7. The vector of claim 4 wherein the spacer region is located in an inverted repeat of the chloroplast genome.

8. The vector of claim 5 wherein the spacer region is located in an inverted repeat of the chloroplast genome.

9. The vector of claim 6 wherein the spacer region is located in an inverted repeat of the chloroplast genome.

10. The vector of claim 4 which comprises in the spacer region, a chloroplast origin of replication, whereby homoplasmy with the genome is promoted.

11. The vector of claim 5 which comprises in the spacer region, a chloroplast origin of replication, whereby homoplasmy with the genome is promoted.

12. The vector of claim 6 which comprises in the spacer region, a chloroplast origin of replication, whereby homoplasmy with the genome is promoted.

13. The vector of claim 7 which comprises in the spacer region, a chloroplast origin of replication, whereby homoplasmy with the genome is promoted.

14. The vector of claim 8 which comprises in the spacer region, a chloroplast origin of replication, whereby homoplasmy with the genome is promoted.

15. The vector of claim 9 which comprises in the spacer region, a chloroplast origin of replication, whereby homoplasmy with the genome is promoted.

16. The vector of claim 4 wherein the DNA of the flanking sequences originate from a plant species other than that of the target plant.

17. The vector of claim 5 wherein the DNA of the flanking sequences originate from a plant species other than that of the target plant.

18. The vector of claim 6 wherein the DNA of the flanking sequences originate from a plant species other than that of the target plant.

19. The vector of claim 7 wherein the DNA of the flanking sequences originate from a plant species other than that of the target plant.

20. The vector of claim 8 wherein the DNA of the flanking sequences originate from a plant species other than that of the target plant.

21. The vector of claim 9 wherein the DNA of the flanking sequences originate from a plant species other than that of the target plant.

22. The vector of claim 10 wherein the DNA of the flanking sequences originate from a plant species other than that of the target plant.

23. The vector of claim 11 wherein the DNA of the flanking sequences originate from a plant species other than that of the target plant.

24. The vector of claim 12 wherein the DNA of the flanking sequences originate from a plant species other than that of the target plant.

25. The vector of claim 13 wherein the DNA of the flanking sequences originate from a plant species other than that of the target plant.

26. The vector of claim 14 wherein the DNA of the flanking sequences originate from a plant species other than that of the target plant.

27. The vector of claim 15 wherein the DNA of the flanking sequences originate from a plant species other than that of the target plant.

28. The vector of claim 13 wherein the DNA of the flanking sequences originate from a plant other than the target plant from the same plant species as the target plant species.

29. The vector of claim 14 wherein the DNA of the flanking sequences originate from a plant other than the target plant from the same plant species as the target plant species.

30. The vector of claim 15 wherein the DNA of the flanking sequences originate from a plant other than the target plant from the same plant species as the target plant species.

31. A stably transformed plant which comprises chloroplast stably transformed with the vector of claim 4, or the progeny thereof.

32. A stably transformed plant which comprises chloroplast stably transformed with the vector of claim 5, or the progeny thereof.

33. A stably transformed plant which comprises chloroplast stably transformed with the vector of claim 6, or the progeny thereof.

34. A stably transformed plant which comprises chloroplast stably transformed with the vector of claim 7, or the progeny thereof.

35. A stably transformed plant which comprises chloroplast stably transformed with the vector of claim 8, or the progeny thereof.

36. A stably transformed plant which comprises chloroplast stably transformed with the vector of claim 9, or the progeny thereof.

37. A stably transformed plant which comprises chloroplast stably transformed with the vector of claim 10, or the progeny thereof.

38. A stably transformed plant which comprises chloroplast stably transformed with the vector of claim 11, or the progeny thereof.

39. A stably transformed plant which comprises chloroplast stably transformed with the vector of claim 12, or the progeny thereof.

40. A stably transformed plant which comprises chloroplast stably transformed with the vector of claim 25, or the progeny thereof.

41. A stably transformed plant which comprises chloroplast stably transformed with the vector of claim 26, or the progeny thereof.

42. A stably transformed plant which comprises chloroplast stably transformed with the vector of claim 27, or the progeny thereof.

43. A stably transformed plant which comprises chloroplast stably transformed with the vector of claim 28, or the progeny thereof.

44. A stably transformed plant which comprises chloroplast stably transformed with the vector of claim 29, or the progeny thereof.

45. A stably transformed plant which comprises chloroplast stably transformed with the vector of claim 30, or the progeny thereof.

46. The stably transformed plant of claim 31 which is a solanaceous plant.

47. The stably transformed plant of claim 32 which is a solanaceous plant.

48. The stably transformed plant of claim 33 which is a solanaceous plant.

49. The stably transformed plant of claim 40 which is a solanaceous plant.

50. The stably transformed plant of claim 41 which is a solanaceous plant.

51. The stably transformed plant of claim 42 which is a solanaceous plant.

52. The stably transformed plant of claim 31, which is monocotyledonous.

53. The stably transformed plant of claim 32, which is monocotyledonous.

54. The stably transformed plant of claim 33, which is monocotyledonous.

55. The stably transformed plant of claim 31 which is dicotyledonous.

56. The stably transformed plant of claim 32 which is dicotyledonous.

57. The stably transformed plant of claim 33 which is dicotyledonous.

58. The stably transformed plant of claim 34 which is monocotyledonous.

59. The stably transformed plant of claim 35 which is monocotyledonous.

60. The stably transformed plant of claim 36 which is monocotyledonous.

61. The stably transformed plant of claim 34 which is dicotyledonous.

62. The stably transformed plant of claim 35 which is dicotyledonous.

63. The stably transformed plant of claim 36 which is dicotyledonous.

64. The stably transformed plant of claim 37 which is monocotyledonous.

65. The stably transformed plant of claim 38 which is monocotyledonous.

66. The stably transformed plant of claim 39 which is monocotyledonous.

67. The stably transformed plant of claim 37 which is dicotyledonous.

68. The stably transformed plant of claim 38 which is dicotyledonous.

69. The stably transformed plant of claim 39 which is dicotyledonous.

70. The stably transformed plant of claim 40 which is monocotyledonous.

71. The stably transformed plant of claim 41 which is monocotyledonous.

72. The stably transformed plant of claim 42 which is monocotyledonous.

73. The stably transformed plant of claim 64 which is maize, rice, grass, rye, barley, oat or wheat.

74. The stably transformed plant of claim 65 which is maize, rice, grass, rye, barley, oat or wheat.

75. The stably transformed plant of claim 66 which is maize, rice, grass, rye, barley, oat or wheat.

76. The stably transformed plant of claim 67 which is soybean, peanut, grape, potato, sweet potato, pea, canola, tobacco, tomato or cotton.

77. The stably transformed plant of claim 68 which is soybean, peanut, grape, potato, sweet potato, pea, canola, tobacco, tomato or cotton.

78. The stably transformed plant of claim 69 which is soybean, peanut, grape, potato, sweet potato, pea, canola, tobacco, tomato or cotton.

79. The stably transformed plant of claim 70 which is maize, rice, grass, rye, barley, oat or wheat.

80. The stably transformed plant of claim 71 which is maize, rice, grass, rye, barley, oat or wheat.

81. The stably transformed plant of claim 72 which is maize, rice, grass, rye, barley, oat or wheat.

82. The stably transformed plant of claim 67 which is soybean, peanut, grape, potato, sweet potato, pea, canola, tobacco, tomato or cotton.

83. The stably transformed plant of claim 68 which is soybean, peanut, grape, potato, sweet potato, pea, canola, tobacco, tomato or cotton.

84. The stably transformed plant of claim 69 which is soybean, peanut, grape, potato, sweet potato, pea, canola, tobacco, tomato or cotton.

85. A process for stably transforming a target plant species which comprises introducing an integration and expression universal vector into the chloroplast genome of the target plant and allowing the transformed plant to grow, the vector being competent to stably transform the chloroplast of different plant species and comprising an expression cassette which comprises, operably joined, a heterologous DNA sequence coding for a molecule of interest and control sequences positioned upstream from the 5' and downstream from the 3' ends of the coding sequence to provide expression of the coding sequence in the chloroplast of the target plant, a heterologous sequence coding for a selectable phenotype, and flanking each side of the expression cassette, flanking DNA sequences which comprise each one a portion of the intergenic spacer 2 region between the $tRNA^{Ile}$ and the $tRNA^{Ala}$ genes of the chloroplast genome, which are homologous to a spacer sequence of the target chloroplast genome, which sequence is conserved in the chloroplast genome of different plants species, whereby stable integration of the heterologous coding sequence into the chloroplast genome of the target plant is facilitated through homologous recombination of the flanking sequences with the homologous sequences in the target chloroplast genome.

86. A process for stably transforming a target plant species which comprises introducing an integration and expression universal vector into the chloroplast genome of the target plant species and allowing the transformed plant to grow, the vector being competent to stably transform the

chloroplast of different plants species and comprising an expression cassette which comprises, operably joined, a heterologous DNA sequence coding for a peptide of interest, and control sequences positioned upstream from the 5' and downstream from the 3' ends of the coding sequence to provide expression of the coding sequence in the chloroplast of the target plant, a heterologous nucleotide sequence coding for a selectable phenotype, and flanking each side of the expression cassette, flanking DNA sequences which comprise each one a portion of the intergenic spacer 2 region between the $tRNA^{Ile}$ and the $tRNA^{Ala}$ genes of the chloroplast genome, which are homologous to a spacer sequence of the target chloroplast genome, which sequence is conserved in the chloroplast genome of different plant species, whereby stable integration of the heterologous coding sequence into the chloroplast genome of the target plant is facilitated through homologous recombination of the flanking sequences with the homologous sequences in the target chloroplast genome.

87. The process of claim 86 wherein the transformed plant is heteroplasmic.

88. The process of claim 86 wherein the transformed plant is a homoplasmic plant.

89. The process of claim 88 wherein the transformed plant is a first generation plant.

90. The process of claim 86 wherein the target plant is a solanaceous plant.

91. The process of claim 86 wherein the transformed plant is monocotyledonous.

92. The process of claim 86 wherein the transformed plant is dicotyledonous.

93. The process of claim 91 wherein the transformed plant is one of the following monocotyledonous plants: maize, rice, grass, rye, barley, oat or wheat.

94. The process of claim 92 wherein the transformed plant is one of the following dicotyledonous plants: soybean, peanut, grape, sweet potato, pea, canola, tobacco, tomato or cotton.

95. The process of claim 86 which comprises isolating the peptide of interest.

96. The process of claim 86 wherein the peptide of interest is a polypeptide.

97. The process of claim 96 wherein the polypeptide is a synthetic protein-base polymer (PBP).

98. The process of claim 97 wherein the PBP has repeating pentamer sequences $(GVGVP)_n$ wherein "n" is an integer of 1 to 250, "G" is glycine, "V" is valine and "P" is proline.

99. The process of claim 98 wherein "n" is 121.

100. The process of claim 96 wherein the expressed polypeptide of interest is insulin.

101. The process of claim 100 which comprises isolating the insulin.

102. The process of claim 100 wherein the insulin is in the form of pro-insulin.

103. The process of claim 102 wherein the pro-insulin is fused to a PBP.

104. The process of claim 100 wherein the transformed plant is tobacco.

105. The process of claim 96 wherein the polypeptide of interest is human serum albumin (HSA).

106. The process of claim 105 wherein the transformed plant is tobacco.

107. The vector of claim 4 wherein the peptide of interest is a biologically active molecule.

108. The vector of claim 107 wherein the peptide is a polypeptide which is a synthetic protein-based polymer (PBP).

109. The vector of claim 108 wherein the PBP has repeating pentamer sequences $(GVGVP)_n$ wherein "n" is an integer of 1 to 250, "G" is glycine, "V" is valine and "P" is proline. SEQ ID NO:17

110. The vector of claim 109 wherein the polypeptide is $(GVGVP)_n$ wherein the integer "n" is 121.

111. The vector of claim 108 wherein the PBP is fused to a biologically active molecule.

112. The vector of claim 111 wherein the biologically active molecule is insulin.

113. The vector of claim 112 wherein the insulin is in the form of pro-insulin.

114. The polypeptide obtained by the process of claim 96.

115. The PBP obtained by the process of claim 97.

116. The pro-insulin obtained by the process of claim 102.

117. The HSA obtained by the process of claim 105.

118. A stably transformed plant which comprises a chloroplast genome stably transformed with the vector of claim 107 which comprises a biologically active molecule.

119. The harvested plant of claim 118.

120. The biologically active molecule isolated from the plant of claim 118.

121. The biologically active molecule of claim 120 which is insulin.

122. The stably transformed plant of claim 118 which is tobacco.

123. A stably transformed herbicide resistant target plant species or the progeny thereof, which comprises chloroplast stably transformed with a universal integration and expression vector competent for stable transformation of the chloroplast of different plants species which comprises an expression cassette which comprises a heterologous protein of interest expressed by a heterologous DNA sequence in the chloroplast genome of the target plant species, a selected phenotype other than tolerance to said herbicide, and flanking each side of the expression cassette, flanking DNA sequences which comprise each one a portion of the intergenic spacer 2 region between the $tRNA^{Ile}$ and the $tRNA^{Ala}$ genes of the chloroplast genome, which are homologous to a spacer sequence of the target chloroplast genome, which sequence is conserved in the chloroplast genome of different plant species, whereby stable integration of the heterologous protein into the chloroplast genome of the target plant was facilitated through homologous recombination of the flanking sequences with the homologous sequences in the target chloroplast genome.

124. The herbicide resistant target plant of claim 123 in which the protein of interest is a mutant form of an enzyme which has decreased affinity for the herbicide than does the naturally occurring enzyme.

125. The herbicide resistant target plant of claim 123 wherein the herbicide is glyphosate.

126. The herbicide resistant target plant of claim 125 wherein the enzyme is EPSP synthase.

127. The herbicide resistant target plant of claim 124 wherein the herbicide is selected from at least one of the following types: PSI, PSII, APP, auxin analog, mitotic, tertiary amino methyl phosphoric acids type and ALS inhibiting types.

128. The herbicide resistant target plant of claim 127 wherein the herbicide is the PSI type selected from paraquat and diquat.

129. The herbicide resistant target plant of claim 127 wherein the herbicide is selected from atrazine, dinoseb, lenacil and metribuzine.

130. The herbicide resistant target plant of claim 127 wherein the herbicide is of the APP type selected from cyclohexanedione, haloxyfop, clethodim and phenoxaprop, and the lower alkyl-substituted compound thereof.

131. The herbicide resistant target plant of claim 127 wherein the herbicide is an auxin analog selected from MCPA and 2,4-D.

132. The herbicide resistant target plant of claim 127 wherein the herbicide is a mitotic type herbicide, which is dinitroaniline.

133. The herbicide resistant target plant of claim 124 wherein the herbicide is a tertiary amino methyl phosphoric acid type, which is glyphosate.

134. The herbicide resistant target plant of claim 127 wherein the herbicide is an ALS inhibiting type selected from sulfonylureas and imidazolines.

135. The herbicide resistant target plant of claim 127 wherein the herbicide is selected from bromoxynil, methyl sulfuron, chlorsulfuron, phosphinothricin and imazapyr.

136. The herbicide resistant target plant of claim 123 wherein the expressed phenotype is antibiotic resistance.

137. The herbicide resistant plant of claim 123 wherein the selectable phenotype is encoded by the hygromycin gene that confers herbicide resistance.

138. The herbicide resistant target plant of claim 127 which is maize, rice, grass, rye, barley, oat, wheat, soybean, peanut, grape, potato, sweet potato, pea, canola, tobacco, tomato or cotton.

139. The herbicide resistant target plant of claim 138 which is a homoplasmic plant.

140. A process for conferring herbicide resistance to a target plant species which comprises introducing into the plant a universal integration and expression vector competent for stably transformed with a universal integration and expression vector competent for stably transforming the chloroplast of different plants species which comprises an expression cassette which comprises, operably joined, a heterologous DNA sequence coding for a protein of interest which confers resistance to a herbicide and control sequences positioned upstream from the 5' and downstream from the 3' ends of the coding sequence to provide expression of the coding sequence in the chloroplast of the target plant, a heterologous nucleotide sequence coding for a selectable phenotype other than for tolerance to said herbicide, and flanking each side of the expression cassette, flanking sequences which comprise each one a portion of the intergenic spacer 2 region between the $tRNA^{Ile}$ and the $tRNA^{Ala}$ genes of the chloroplast genome, which are homologous to a spacer sequence of the target chloroplast genome, which sequence is conserved in the chloroplast genome of different plant species, whereby stable integration of the heterologous coding sequence into the chloroplast genome of the target plant is facilitated through homologous recombination of the flanking sequences with the homologous sequences in the target chloroplast genome and growing the transformed plant.

141. The process of claim 140 wherein the DNA sequence codes for a mutant form of an enzyme which has decreased affinity for the herbicide than does the naturally occurring enzyme.

142. The process of claim 141 wherein the enzyme is EPSP synthase and the herbicide is glyphosate.

143. The process of claim 142 wherein DNA sequence is the EPSP synthase gene which is a mutant EPSP synthase gene.

144. The process of claim 140 which comprise selecting the viable, transformed target plants from a medium which is lethal to non-transformed plants.

145. The process of claim 144 wherein the viable transformed target plants are homoplasmic plants.

146. The process of claim 144 wherein the viable transformed target plants are heteroplasmic plants.

147. The process of claim 140 wherein the herbicide resistant target plant is tobacco, the nucleotide sequence codes for a selectable phenotype which is lethal to tobacco or for a visual trait that permits to select the transformed tobacco plants from the non-transformed plants.

148. The process of claim 147 wherein the lethal selectable phenotype is hygromycin to which tobacco is not naturally resistant.

149. The process of claim 147 wherein the visual trait is the expression of a color.

150. The process of claim 140 for stably transforming the phenotype of a target plant species, whereby the grown transformed plant expresses the selectable phenotype and another trait in addition to the expression of that phenotype.

151. The process of claim 150 wherein the selected phenotype is conferred by expression of the hygromycin β-phosphotransferase gene and the additional trait that is conferred is resistance to the herbicide glyphosate.

152. A process of determining chloroplast transformation and expression of a target trait on the basis of a target plant species acquisition of resistance to a selected herbicide due to the transformation of the plant species which comprises introducing into the plant a universal integration and expression vector competent for stably transforming the chloroplast of different plant species which comprises an expression cassette which comprises, operably joined, a heterologous DNA sequence coding for the desired target trait and control sequences positioned upstream from the 5' and downstream from the 3' ends of the coding sequence to provide expression of the coding sequence in the chloroplast of a target plant, a heterologous nucleotide sequence coding for a selectable phenotype and flanking each side of the expression cassette, flanking DNA sequences which comprise each one a portion of the intergenic spacer 2 region between the $tRNA^{Ile}$ and the $tRNA^{Ala}$ genes of the chloroplast genome, which are homologous to a spacer sequence of the target chloroplast genome, which sequence is conserved in the chloroplast genome of different plant species, whereby stable integration of the heterologous coding sequence into the chloroplast genome of the target plant is facilitated through homologous recombination of the flanking sequences with the homologous sequences in the target chloroplast genome, exposing the plants into which the vector has been introduced to a lethal concentration of the herbicide and selecting the plants which do not die from exposure thereto, thereby having selected the transformed plants which express the desired target trait.

153. The process of claim 152 wherein the selected herbicide is selected from at least one of the following types: PSI, PSII, APP, auxin analog, mitotic, tertiary amino methyl phosphoric acids and ALS inhibiting types.

154. A stably transformed insect resistant target plant species or the progeny thereof, which comprises chloroplast genome stably transformed with a universal integration and expression vector competent for stable transformation of the chloroplast of different plants species which comprises an expression cassette which comprises a heterologous DNA sequence which expresses a target protein which confers resistance to a target insect in the chloroplast genome of the target plant species, a selected phenotype other than tolerance to the target insect, and flanking each side of the expression cassette, flanking DNA sequences which comprise each one a portion of the intergenic spacer 2 region between the $tRNA^{Ile}$ and the $tRNA^{Ala}$ genes of the chloroplast genome, which are homologous to a spacer sequence of the target chloroplast genome, which sequence is conserved in the chloroplast genome of different plants species, whereby stable integration of the heterologous protein into the chloroplast genome of the target plant was facilitated through homologous recombination of the flanking sequences with the homologous sequences in the target chloroplast genome, wherein the heterologous protein is the CryIIA protein toxin expressed by the *cry*IIA gene, which protein confers resistance to insects.

155. The stably transformed insect-resistant target plant species of claim 154 wherein the insect is susceptible to the Bt toxin.

156. The stably transformed insect-resistant target plant species of claim 154 wherein the insect's lack of susceptibility to the Bt toxin is overcome.

157. The stably transformed insect-resistant target plant species of claim 155 wherein the target plant is tobacco and the insect is tobacco budworm.

158. The stably transformed insect-resistant target plant species of claim 156 wherein the target plant is tobacco, cotton or beet and the insect is a Bt toxin-resistant type cottonboll worm or beet armyworm.

159. The stably transformed insect-resistant target plant of claim 154 wherein the insect is tobacco budworm, cottonboll worm or beet armyworm.

160. A vector selected from the following: pSBL-RD-EPSPS, pSBL-CG-EG121, pSBL-Ct-Border, pSBL-Ct-V1, pSBL-Ct-V2, pSBL-CtV3, pSBL-Ct-VH, pSBL-Ct-VHF, and pSBL-Ct-VHBt.

161. The vector of claim 160 which is a universal integration and expression vector which is pSBL-RD-EPSPS, pSBL-CG-EG121, pSBL-CtV1, pSBL-CtV2, pSBL-CtV3, pSBL-CtVH, pSBL-Ct-VHF, and pSBL-CtVHBt.

162. An isolated DNA sequence which comprises the intergenic DNA sequence between the 16S and 23S rDNA genes of plant chloroplast genome, which intergenic sequence is highly conserved in a multiplicity of different species of plants.

163. The isolated DNA sequence of claim 162 which comprises the spacer 2 region which is the intergenic DNA sequence between the trnI and the trnA genes of plant chloroplast genome.

164. The isolated intergenic DNA sequence of claim 163 which comprises the trnI and the trnA genes.

165. The isolated DNA sequence of claim 163 which comprises one of the inverted repeats of the chloroplast genome of the plant.

166. The isolated DNA sequence of claim 165 which comprises an origin of replication.

167. The isolated DNA sequence of claim 163 which comprises the rRNA operon in the spacer 2 region.

168. The universal integration and expression vector of claim 4 wherein the spacer 2 region comprises the rRNA operon.

169. The universal integration and expression vector of claim 4 wherein the flanking sequences are synthetic.

170. The herbicide resistant target plant species of claim 85 wherein the DNA sequence which codes for the protein of interest is of prokaryotic origin.

SUB D37 171. The universal integration and expression vector of claim 2 which does not include a transposon.

172. The stably transformed target plant species of claim 41 which does not include a transposon.

173. The process for stably transforming a target plant species of claim 86 wherein the universal vector does not include a transposon.

174. The universal integration and expression vector of claim 4 which comprises a promoter functional in chloroplast.

175. The Universal expression and integration vector of claim 4 which comprises a nucleotide sequence encoding a selectable phenotype which allows for identification and selection of viable transformed plants from non-viable, non-transformed plants.

176. The process of claim 86 which comprises selecting from a medium which is lethal to non-transformed plants, the viable transformed target plant.

177. The stably transformed herbicide tolerant target plant or progeny thereof of claim 123 which allows identification and selection on the basis of viable transformed plants from non-viable, non-transformed plant.

178. The process of claim 140 which comprises selecting from a medium which is lethal to non- transformed plants, the viable transformed target plant.

179. An expression cassette competent for stably transforming chloroplast genome of a target plant which comprises, operably joined, a heterologous DNA sequence coding for a molecule of interest, control sequences to provide expression of the coding sequence in the chloroplast genome of the target plant, a promoter functional in chloroplast, and flanking each side of the cassette, plant DNA sequences to facilitate stable integration of the DNA with the target chloroplast genome by homologous recombination, whereby the DNA is stably integrated therein and is inherited through organelle replication in daughter cells.

180. The expression cassette of claim 175 wherein the heterologous DNA sequence is a synthetic sequence coding for a protein-based polymer (PBP).

181. The expression cassette of claim ~~176~~ 80 wherein the PBP has repeating pentamer sequences $(GVGVP)_n$ wherein "n" is an integer of 1 to 250, "G" is glycine, "V" is valine and "P" is proline.

182. The expression cassette of claim 177 wherein the synthetic coding sequence is the synthetic biopolymer gene EG121 and the expressed PBP is the polymer protein $(GVGVP)_{121}$.

183. A stably transformed transcription/translation active chloroplast genome of a target plant, which is competent for stable integration of a heterologous DNA sequence, which comprises an expression cassette which comprises a heterologous molecule of interest encoded by a heterologous DNA sequence and expressed by control sequences in the chloroplast genome of the target plant, and plant DNA flanking each side of the expression cassette which facilitated stable integration of the DNA into the target chloroplast genome by homologous recombination, which DNA is inherited through organelle replication in daughter cells.

184. The ~~stably transformed chloroplast~~ expression cassette of claim 179 wherein the molecule of interest is a protein-based polymer (PBP).

185. The expression cassette ~~stably transformed chloroplast~~ of claim 180 wherein the PBP has repeating pentamer sequences $(GVGVP)_n$ SEQ ID NO:17 wherein n is an integer of 1 to 250, "G" is glycine, "V" is valine and "P" is proline.

186. The expression cassette ~~stably transformed chloroplast~~ of claim 181 wherein the synthetic coding sequence is the synthetic biopolymer gene EG121 and the expressed PBP is the polymer protein $(GVGVP)_{121}$ SEQ ID NO:17

187. The synthetic biopolymer $(GVGPP)_n$ SEQ ID NO:17 which is expressed from the stably transformed chloroplast of claim 182, wherein "n", "G", "V" and "P" are defined therein.

188. The synthetic biopolymer of claim ~~183~~ 187 which is $(GVGVP)_{121}$ SEQ ID NO:17

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